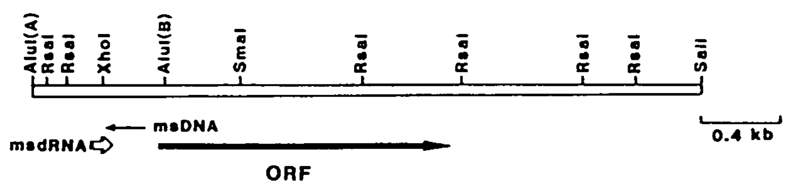

AluI(A)
RsaI
RsaI
XhoI
AluI(B)
SmaI
RsaI
RsaI
RsaI
RsaI
SalI
msDNA
msdRNA
ORF
0.4 kb

FIGURE 1

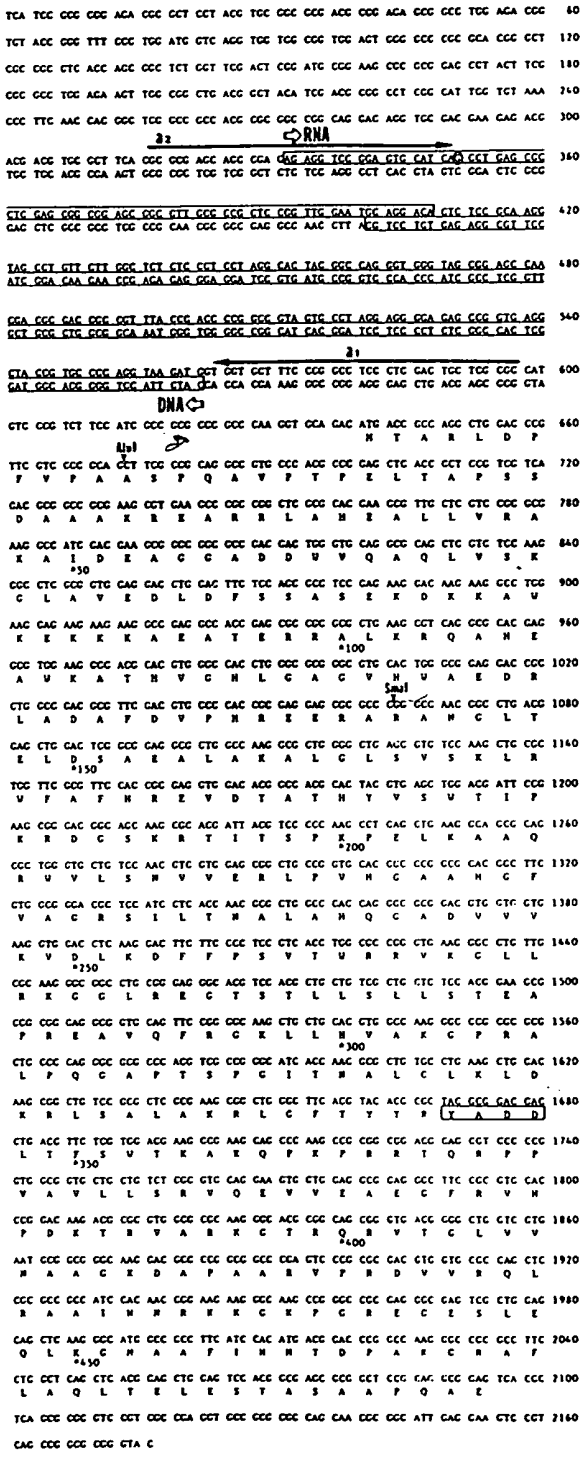


FIGURE 2

```
HIV    RT   VKLKPGMDGPKVKQ  WPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWR
HTLV1  RT   RPWARTPPKAPRNQ PVPFKPERLQALQHLVRKALEACHIEPYTG  PGNNPVFPVKKA NGTWR
Ec-67  RT   NVLYRIGSDNQYTQFTIPKKGKGVRTISAPTDRL KDIQRRICDLLSDCRDEIFAIRKI SNNYS
Mx-162 RT   AFHREVDTATHYVSWTIPKRDGSKRTITSPKPEL KAAQR   WVLS    NVV ERLP VHGAA
                       o   oo•o     ooo  o   o o  oo     oo        o
                                            x  xx              x

HIV    RT   KLVDFRELNKRTQDFWEVQLGIPHPAGLKKK KSVTVLDVGDAYFSVPLDEDFRKYT       A
HTLV1  RT   FIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTIDLRDAFFQIPLPKQFQPYF       A
Ec-67  RT   FGFE RGKSIILNAYKHRGKQIILNIDLKDFFESFNFGRVRG YFLS  NQDF           L
Mx-162 RT   HGFV AGRSILTNALAHQGADVVVKVDLKDFFPSVTWRRVKGLLRKGGLREGTSTLLSLLSTEAP
             oo   o oo  oo  o o       o•oooo o   oo o
                      xx  x             x    xxx  x        x x

HIV    RT   FTIP SINNETPGIRYQYNVLPQGWKGSPAIFQS   SMTKILEPFKKQNPDIVIYQYMDDLYVG
HTLV1  RT   FTVP QQCNYGPGTRYAWKVLPQGFKNSPTLFEM   QLAHILQPIRQAFPQCTILQYMDDILLA
Ec-67  RT   LN PVVATTLAKAACYN GTLPQGSPCSPIISNLICNIHDMRLAKLAKKY GCTYSRYADDITI
Mx-162 RT   REAVQFRGKLLHVAKGP RALPQGAPTSPGITNALCLKLDKRLSALAKRL GFTYTRYADDLTF
                     o   o      •••• o •• o o  o  o o•  ooo   o oo o•o•• o
                                          x      x x      x     x       x

HIV    RT   S DLEIGQHRTKIEELRQHLLRWGLTTP DKKHQKEP PFLWMGYELHPDKWTVQPIVLPE  KD
HTLV1  RT   S  PSHEDLLLLLSEATMASLISHGLPVS ENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPI RS
Ec-67  RT   STNKNTFPLEMATVQPEGVVLGKVLVKEIENSGFEINDSKTRLTYKTSRQEVT GLTVNRIVNID
Mx-162 RT   SWTKAKQPKPRRTQRPPVAVLLSRVQEVVEAEGFRVHPDKTRVARKGTRQRVT GLVVNAAGKDA
            •  o   o    o  o   oo       o  oo     ooo   o  oo o• oo oo
                                x       x                          xx

HIV    RT   SWTVNDIQKLVGKLNWASQIYP
HTLV1  RT   RWALPELQALLGEIQWVSKGTP
Ec-67  RT   RCYYKKTRALAHALYRTGE YK
Mx-162 RT   PAARVPRDVVRQLRAAIHN RK
                                 o
              x
```

FIGURE 3

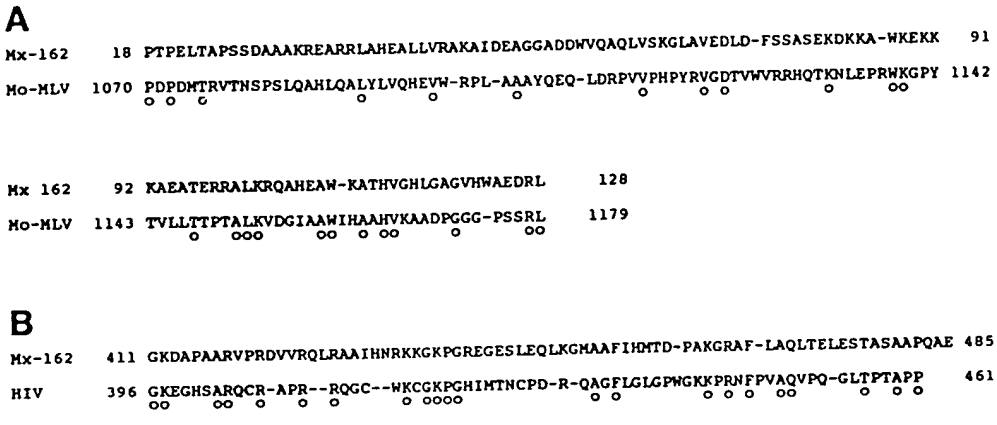


Figure 4. Sequence Similarity of the msDNA-Mx162 Reverse Transcriptase with Other Retroelements

(A) Sequence similarity of the region from residues 18 to 128 of the msDNA Mx162 RT (see Figure 2) with a carboxy-terminal region of integration protein of Moloney murine leukemia virus (M-MuLV) (residues 1070 to 1179; Shinnick et al., 1981)

(B) Comparison of the sequence from residues 411 to 485 of the msDNA-Mx162 RT (see Figure 2) with the sequence from residues 396 to 461 of the *gag* protein of human immunodeficiency virus (HIV; Ratner et al., 1985).

FIGURE 4

A

```
Mx-162       304  GP-RALPQGAPTSPGITNALCLKLDKRLSALAKRL-GFTYTRYADDLTF-SWTKAKQPKPRRTQRPPVAVL  371
Ec-67        159  YN-GTLPQGSPCSPIISNLICNIMDMRLAKLAKKY-GCTYSRYADDITI-STNKNTFPLEMATVQPEGVVL  226
Ec-86        130  YK-NLLPQGAPSSPKLANLICSKLDYRIQGYAGSR-GLIYTRYADDLTL-SAQSMKKVVKARDFLFSIIPS  197
HIV          311  YQYNVLPQGWKGSPAIFQS---SMTKILEPFKKQNPDIVIYQYMDDLYVGS-DLEIGQHRTKIEELRQHLL  377
HTLV1        150  YAWKVLPQGFKNSPTLFEM---QLAHILQPIRQAFPQCTILQYMDDILLAS--PSHEDLLLLSEATMASLI  215
Mo-MLV       303  LTWTRLPQGFKNSPTLFDE---ALHRDLADFRIQHPDLILLQYVDDLLLAA-TSELDCQQG-TRALL-QTL  367
RSV          141  FQWKVLPQGMTCSPTICQL---VVGQVLEPLRLKHPSLCMLHYMDDLLLAA--SSHDGLEAAGEEVI-STL  205
BLV          122  FAWRVLPQGFINSPALFER---ALQEPLRQVSAAFSQSLLVSYMDDILYAS--PTEEQRSQCYQALA-ARL  186
Mt.plasmid   288  IATNGVPQGASTSCGLATYNVL-------ELFLRY--DELIMYADDGIL-CRQDPSTPDFSVEEAGVVQEP  348
17.6         339  YEYLRMPFGLKNAP-ATFQRCMN-DI----LRPLLNKHC-LVYLDDIIVFS-TSLDEHLQSLGLVFE--KL  399
GYPSY        284  YEFCRLPFGLRNASSIFQR---ALDDV---LREQI-GKICYVYVDDVIIFS--ENESDHVRHIDTVLK-CL  344
Copia       1032  CKLNKAIYGLKQAARCWFR-CIYI---LDKGNINENIYV-LLYVDDVVIAT--GDMTRMNNFKRYLME-KF 1112
Tal-3        990  CLLKKSLYGLKQSPRQWNA-CVYV-KQVSE-QEHLYL---LLYVDDMLIAG--KSKSEINKVKEQLSM-EF 1069
Ty912        948  IRLKKSLYELKQS-GANWYE--EVRG-WSCVFKNSQV-TICLFVDDMVLFS--KNLNSNKRIIEKLKM-QY 1023
```

B

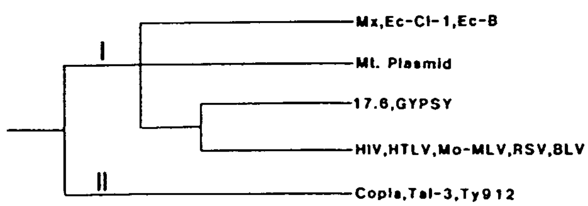


FIGURE 5

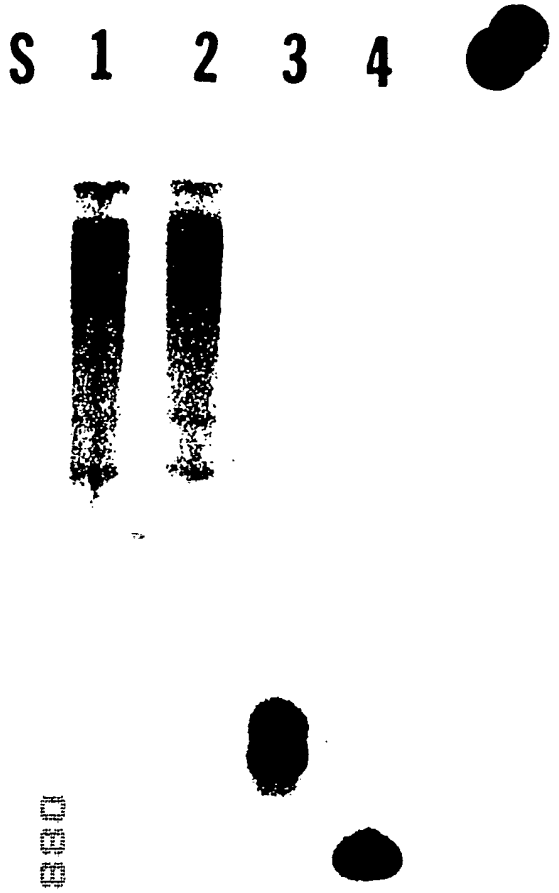


FIGURE 6

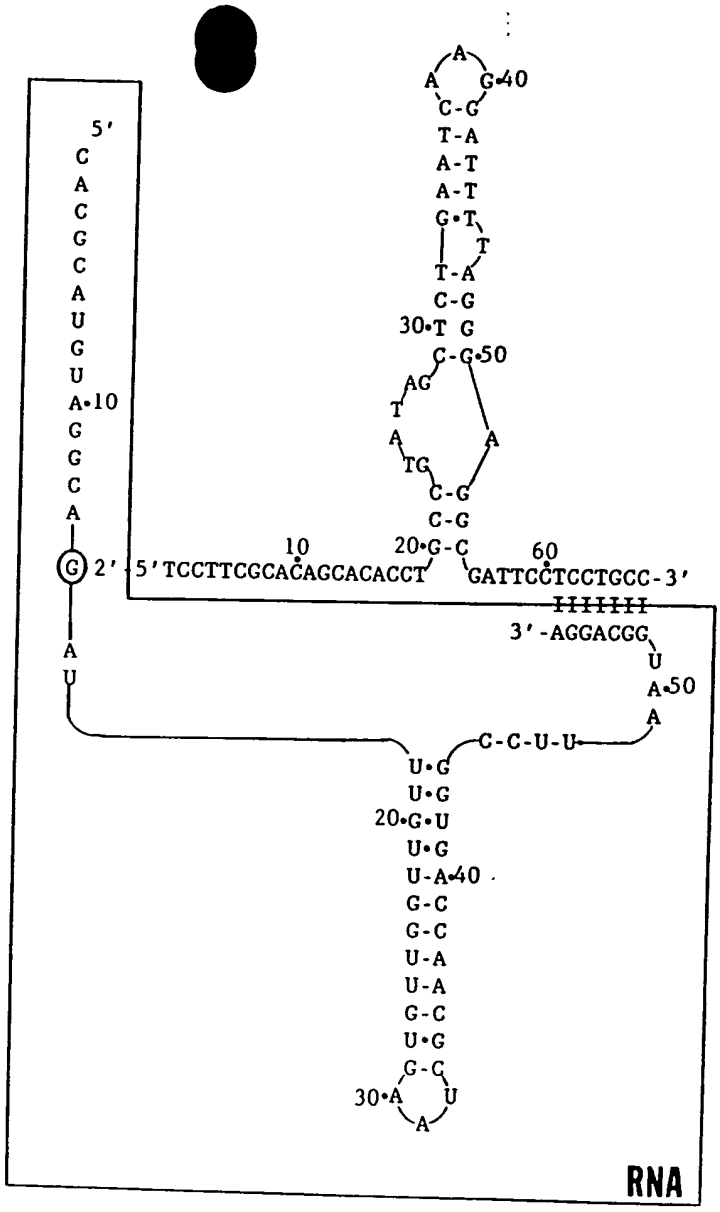
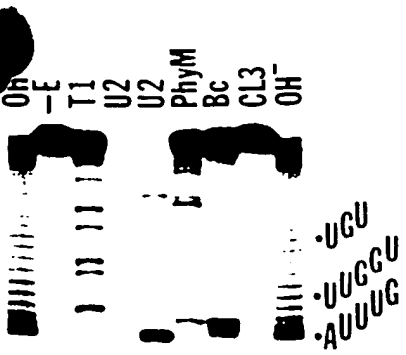


FIGURE 7



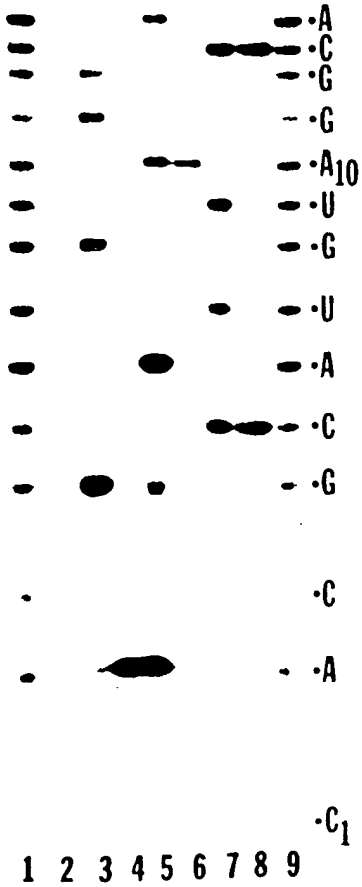
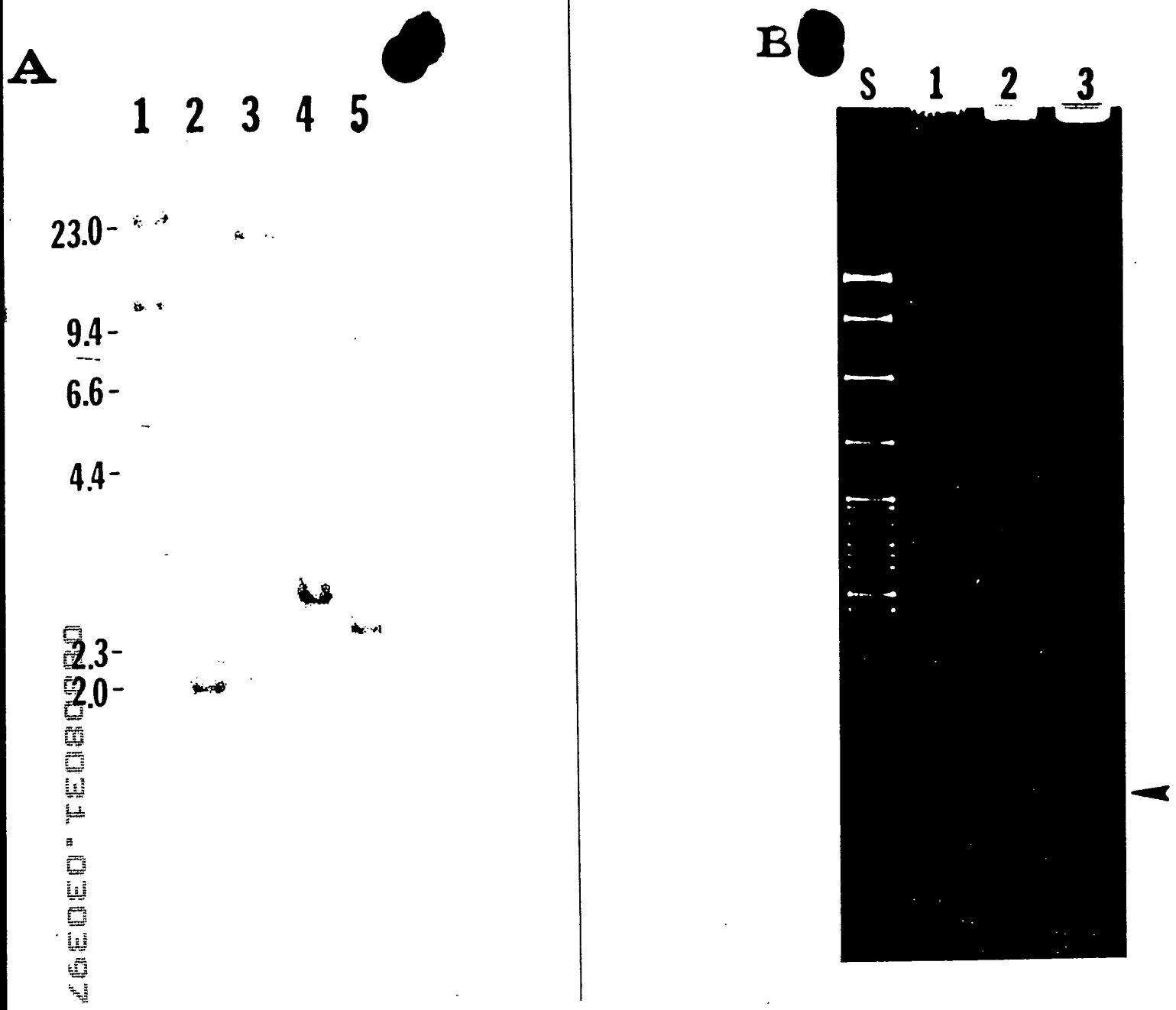


FIGURE 8



FIGU

FIGURE 9

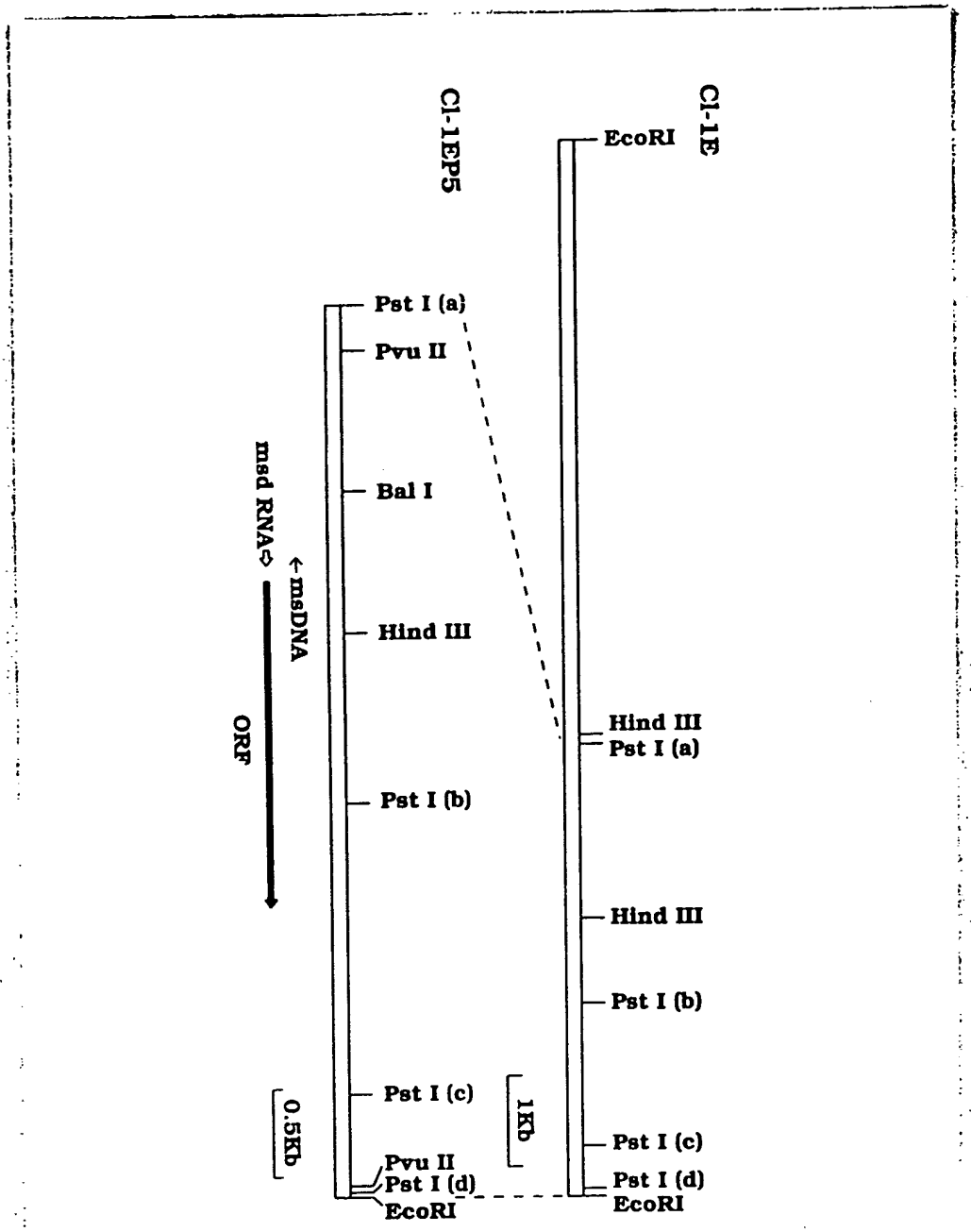

Cl-1EP5
Cl-1E
EcoRI
Pst I (a)
Pvu II
Bal I
Hind III
Pst I (b)
Pst I (c)
Pvu II
Pst I (d)
EcoRI
msd RNA⇨
←msDNA
ORF
0.5Kb
1Kb
Hind III
Pst I (a)
Hind III
Pst I (b)
Pst I (c)
Pst I (d)
EcoRI

FIGURE 10

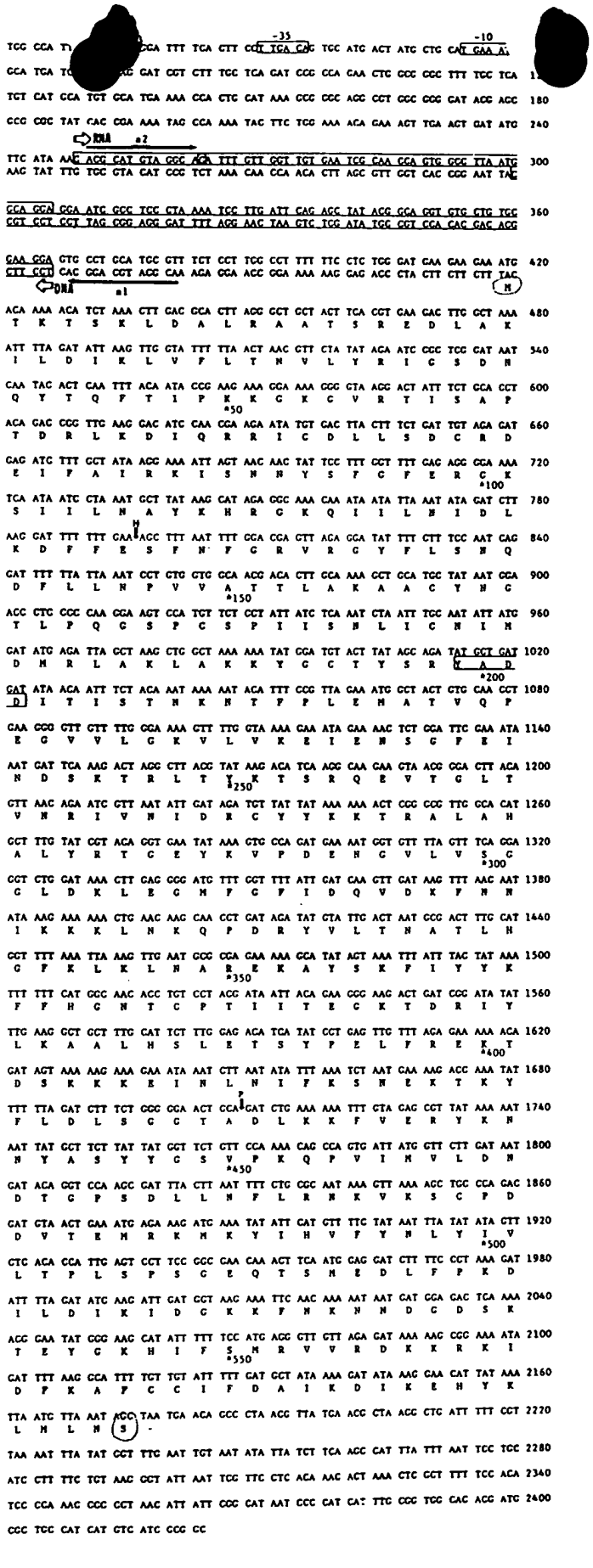


FIGURE 11

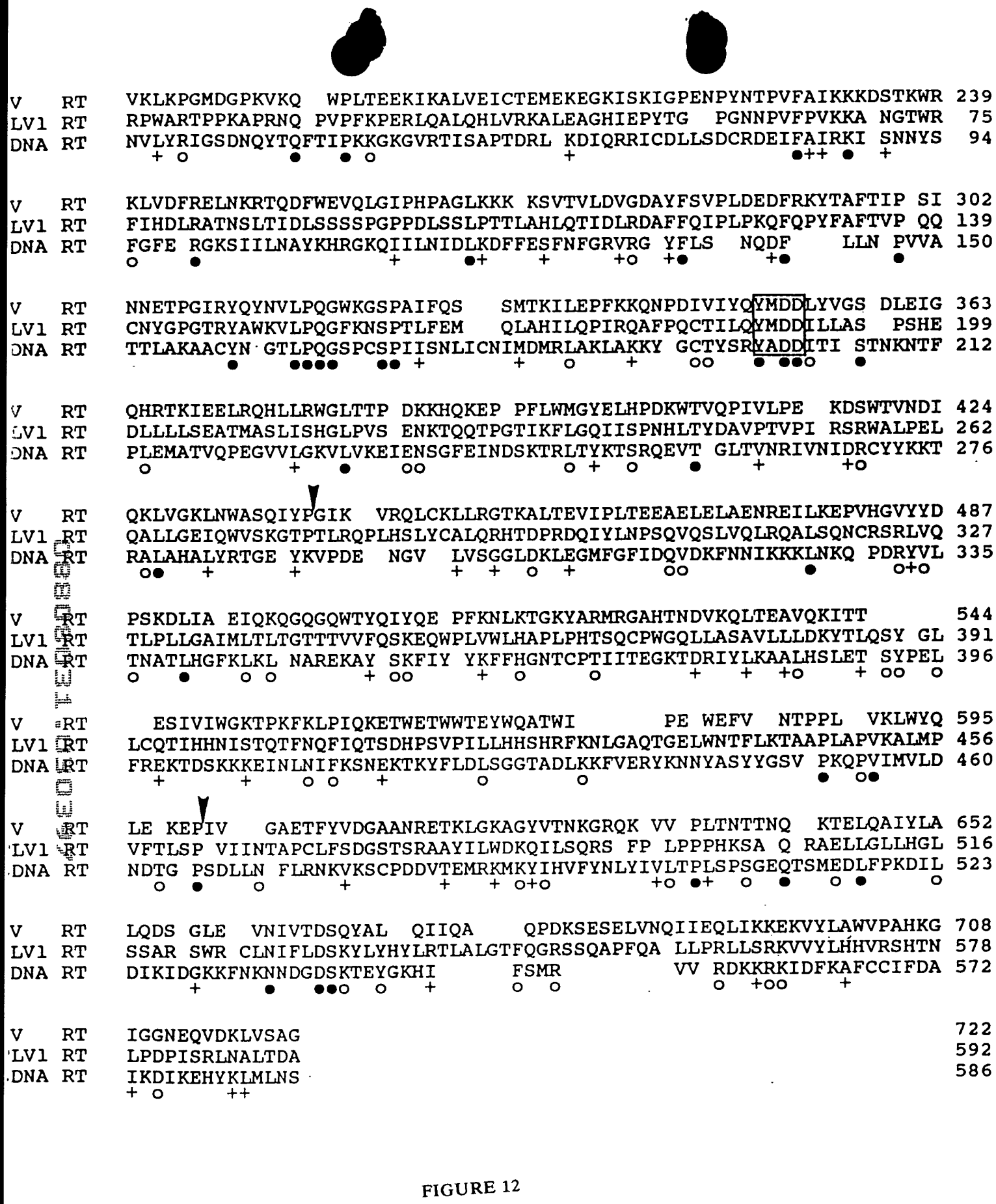

V RT VKLKPGMDGPKVKQ WPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWR 239
LV1 RT RPWARTPPKAPRNQ PVPFKPERLQALQHLVRKALEAGHIEPYTG PGNNPVFPVKKA NGTWR 75
DNA RT NVLYRIGSDNQYTQFTIPKKGKGVRTISAPTDRL KDIQRRICDLLSDCRDEIFAIRKI SNNYS 94
V RT KLVDFRELNKRTQDFWEVQLGIPHPAGLKKK KSVTVLDVGDAYFSVPLDEDFRKYTAFTIP SI 302
LV1 RT FIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTIDLRDAFFQIPLPKQFQPYFAFTVP QQ 139
DNA RT FGFE RGKSIILNAYKHRGKQIILNIDLKDFFESFNFGRVRG YFLS NQDF LLN PVVA 150
V RT NNETPGIRYQYNVLPQGWKGSPAIFQS SMTKILEPFKKQNPDIVIYQYMDDLYVGS DLEIG 363
LV1 RT CNYGPGTRYAWKVLPQGFKNSPTLFEM QLAHILQPIRQAFPQCTILQYMDDILLAS PSHE 199
DNA RT TTLAKAACYN GTLPQGSPCSPIISNLICNIMDMRLAKLAKKY GCTYSRYADDITI STNKNTF 212
V RT QHRTKIEELRQHLLRWGLTTP DKKHQKEP PFLWMGYELHPDKWTVQPIVLPE KDSWTVNDI 424
LV1 RT DLLLLSEATMASLISHGLPVS ENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPI RSRWALPEL 262
DNA RT PLEMATVQPEGVVLGKVLVKEIENSGFEINDSKTRLTYKTSRQEVT GLTVNRIVNIDRCYYKKT 276
V RT QKLVGKLNWASQIYPGIK VRQLCKLLRGTKALTEVIPLTEEAELELAENREILKEPVHGVYYD 487
LV1 RT QALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQLRQALSQNCRSRLVQ 327
DNA RT RALAHALYRTGE YKVPDE NGV LVSGGLDKLEGMFGFIDQVDKFNNIKKKLNKQ PDRYVL 335
V RT PSKDLIA EIQKQGQGQWTYQIYQE PFKNLKTGKYARMRGAHTNDVKQLTEAVQKITT 544
LV1 RT TLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSY GL 391
DNA RT TNATLHGFKLKL NAREKAY SKFIY YKFFHGNTCPTIITEGKTDRIYLKAALHSLET SYPEL 396
V RT ESIVIWGKTPKFKLPIQKETWETWWTEYWQATWI PE WEFV NTPPL VKLWYQ 595
LV1 RT LCQTIHHNISTQTFNQFIQTSDHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMP 456
DNA RT FREKTDSKKKEINLNIFKSNEKTKYFLDLSGGTADLKKFVERYKNNYASYYGSV PKQPVIMVLD 460
V RT LE KEPIV GAETFYVDGAANRETKLGKAGYVTNKGRQK VV PLTNTTNQ KTELQAIYLA 652
LV1 RT VFTLSP VIINTAPCLFSDGSTSRAAYILWDKQILSQRS FP LPPPHKSA Q RAELLGLLHGL 516
DNA RT NDTG PSDLLN FLRNKVKSCPDDVTEMRKMKYIHVFYNLYIVLTPLSPSGEQTSMEDLFPKDIL 523
V RT LQDS GLE VNIVTDSQYAL QIIQA QPDKSESELVNQIIEQLIKKEKVYLAWVPAHKG 708
LV1 RT SSAR SWR CLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQA LLPRLLSRKVVYLHHVRSHTN 578
DNA RT DIKIDGKKFNKNNDGDSKTEYGKHI FSMR VV RDKKRKIDFKAFCCIFDA 572
V RT IGGNEQVDKLVSAG 722
LV1 RT LPDPISRLNALTDA 592
DNA RT IKDIKEHYKLMLNS 586

FIGURE 12

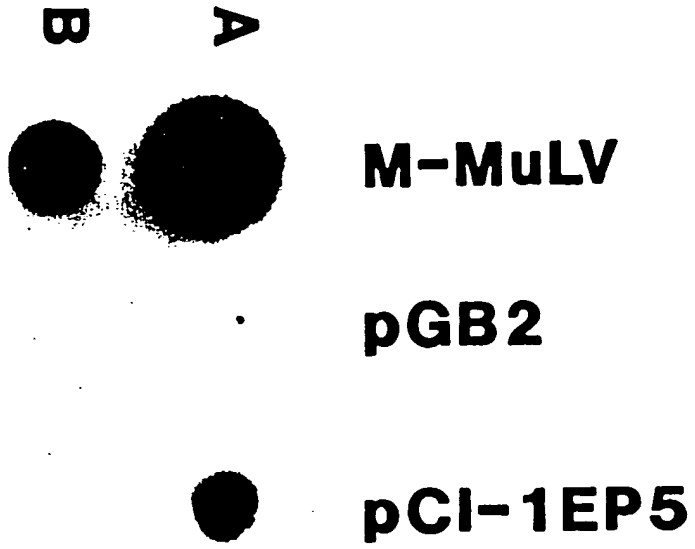


FIGURE 13

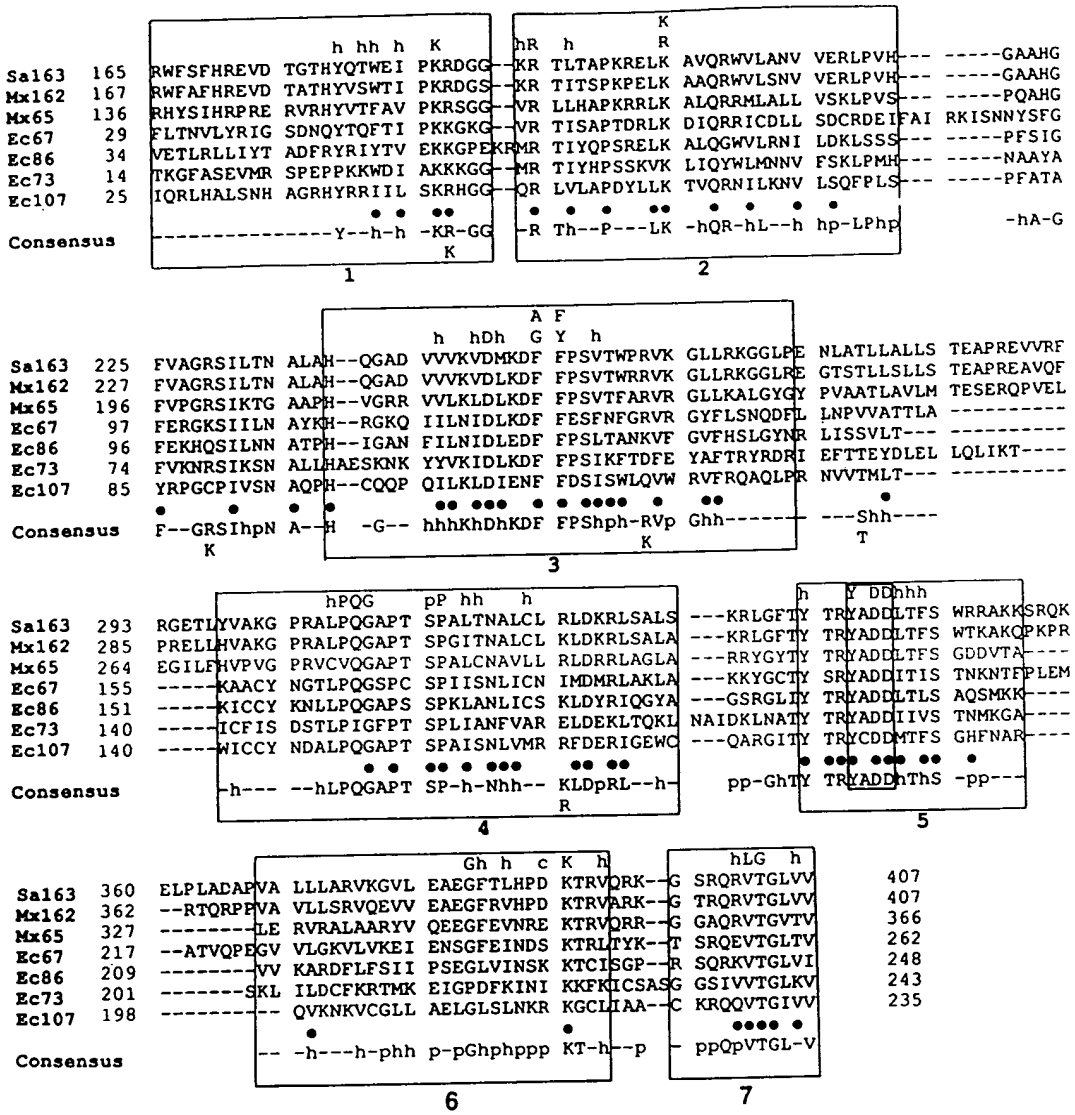

Sa163 165 RWFSFHREVD TGTHYQTWEI PKRDGG--KR TLTAPKRELK AVQRWVLANV VERLPVH--- -----GAAHG
Mx162 167 RWFAFHREVD TATHYVSWTI PKRDGS--KR TITSPKPELK AAQRWVLSNV VERLPVH--- -----GAAHG
Mx65 136 RHYSIHRPRE RVRHYVTFAV PKRSGG--VR LLHAPKRRLK ALQRRMLALL VSKLPVS--- -----PQAHG
Ec67 29 FLTNVLYRIG SDNQYTQFTI PKKGKG--VR TISAPTDRLK DIQRRICDLL SDCRDEIFAI RKISNNYSFG
Ec86 34 VETLRLLIYT ADFRYRIYTV EKKGPEKRMR TIYQPSRELK ALQGWVLRNI LDKLSSS--- -----PFSIG
Ec73 14 TKGFASEVMR SPEPPKKWDI AKKKGG--MR TIYHPSSKVK LIQYWLMNNV FSKLPMH--- -----NAAYA
Ec107 25 IQRLHALSNH AGRHYRRIIL SKRHGG--QR LVLAPDYLLK TVQRNILKNV LSQFPLS--- -----PFATA
Consensus -hA-G
1
2
Sa163 225 FVAGRSILTN ALAH--QGAD VVVKVDMKDF FPSVTWPRVK GLLRKGGLPE NLATLLALLS TEAPREVVRF
Mx162 227 FVAGRSILTN ALAH--QGAD VVVKVDLKDF FPSVTWRRVK GLLRKGGLRE GTSTLLSLLS TEAPREAVQF
Mx65 196 FVPGRSIKTG AAPH--VGRR VVLKLDLKDF FPSVTFARVR GLLKALGYGY PVAATLAVLM TESERQPVEL
Ec67 97 FERGKSIILN AYKH--RGKQ IILNIDLKDF FESFNFGRVR GYFLSNQDFL LNPVVATTLA ----------
Ec86 96 FEKHQSILNN ATPH--IGAN FILNIDLEDF FPSLTANKVF GVFHSLGYNR LISSVLT--- ----------
Ec73 74 FVKNRSIKSN ALLHAESKNK YYVKIDLKDF FPSIKFTDFE YAFTRYRDRI EFTTEYDLEL LQLIKT----
Ec107 85 YRPGCPIVSN AQPH--CQQP QILKLDIENF FDSISWLQVW RVFRQAQLPR NVVTMLT--- ----------
Consensus F--GRSIhpN A--H -G-- hhhKhDhKDF FPShph-RVp Ghh------- ---Shh----
3
Sa163 293 RGETLYVAKG PRALPQGAPT SPALTNALCL RLDKRLSALS ---KRLGFTY TRYADDLTFS WRRAKKSRQK
Mx162 285 PRELLHVAKG PRALPQGAPT SPGITNALCL KLDKRLSALA ---KRLGFTY TRYADDLTFS WTKAKQPKPR
Mx65 264 EGILFHVPVG PRVCVQGAPT SPALCNAVLL RLDRRLAGLA ---RRYGYTY TRYADDLTFS GDDVTA----
Ec67 155 -----KAACY NGTLPQGSPC SPIISNLICN IMDMRLAKLA ---KKYGCTY SRYADDITIS TNKNTFPLEM
Ec86 151 -----KICCY KNLLPQGAPS SPKLANLICS KLDYRIQGYA ---GSRGLIY TRYADDLTLS AQSMKK----
Ec73 140 -----ICFIS DSTLPIGFPT SPLIANFVAR ELDEKLTQKL NAIDKLNATY TRYADDIIVS TNMKGA----
Ec107 140 -----WICCY NDALPQGAPT SPAISNLVMR RFDERIGEWC ---QARGITY TRYCDDMTFS GHFNAR----
Consensus -h--- --hLPQGAPT SP-h-Nhh-- KLDpRL--h- pp-GhTY TRYADDhThS -pp---
4
5
Sa163 360 ELPLADAPVA LLLARVKGVL EAEGFTLHPD KTRVQRK--G SRQRVTGLVV 407
Mx162 362 --RTQRPPVA VLLSRVQEVV EAEGFRVHPD KTRVARK--G TRQRVTGLVV 407
Mx65 327 --------LE RVRALAARYV QEEGFEVNRE KTRVQRR--G GAQRVTGVTV 366
Ec67 217 --ATVQPEGV VLGKVLVKEI ENSGFEINDS KTRLTYK--T SRQEVTGLTV 262
Ec86 209 --------VV KARDFLFSII PSEGLVINSK KTCISGP--R SQRKVTGLVI 248
Ec73 201 -------SKL ILDCFKRTMK EIGPDFKINI KKFKICSASG GSIVVTGLKV 243
Ec107 198 ---------- QVKNKVCGLL AELGLSLNKR KGCLIAA--C KRQQVTGIVV 235
Consensus -- -h---h-phh p-pGhphppp KT-h--p - ppQpVTGL-V
6
7

FIGURE 14

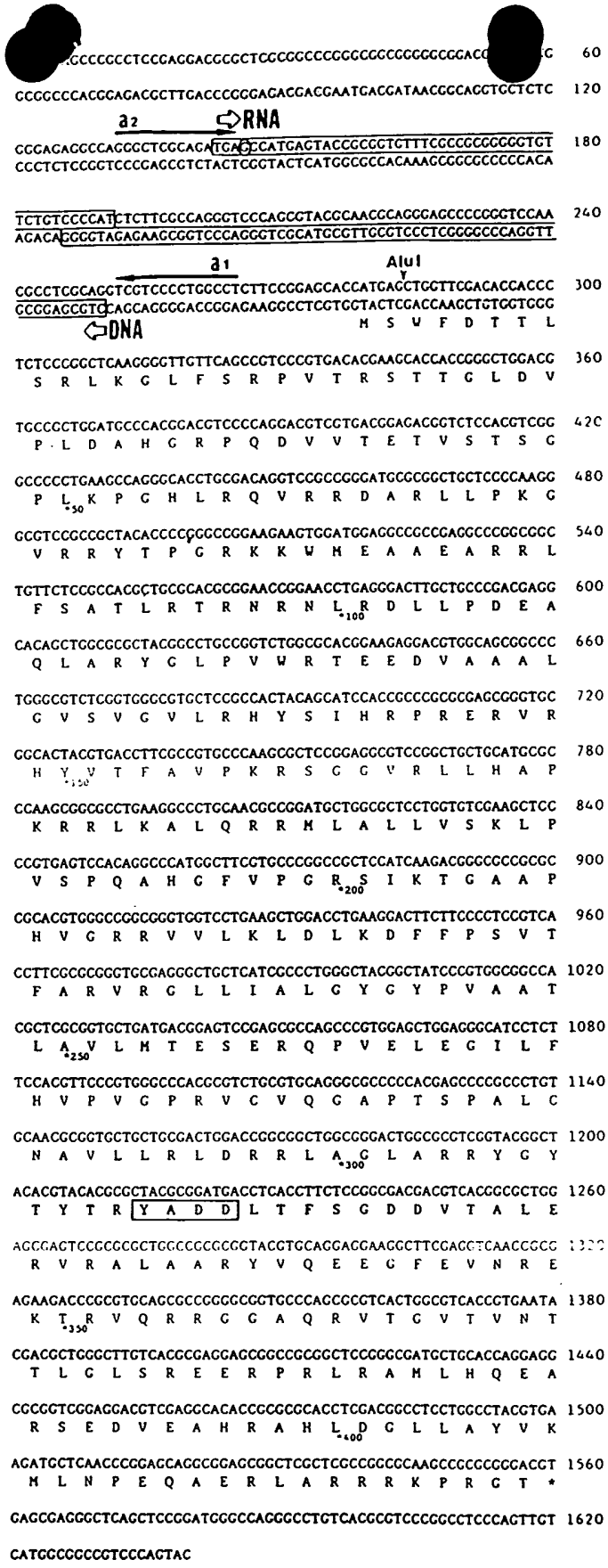


FIGURE 15

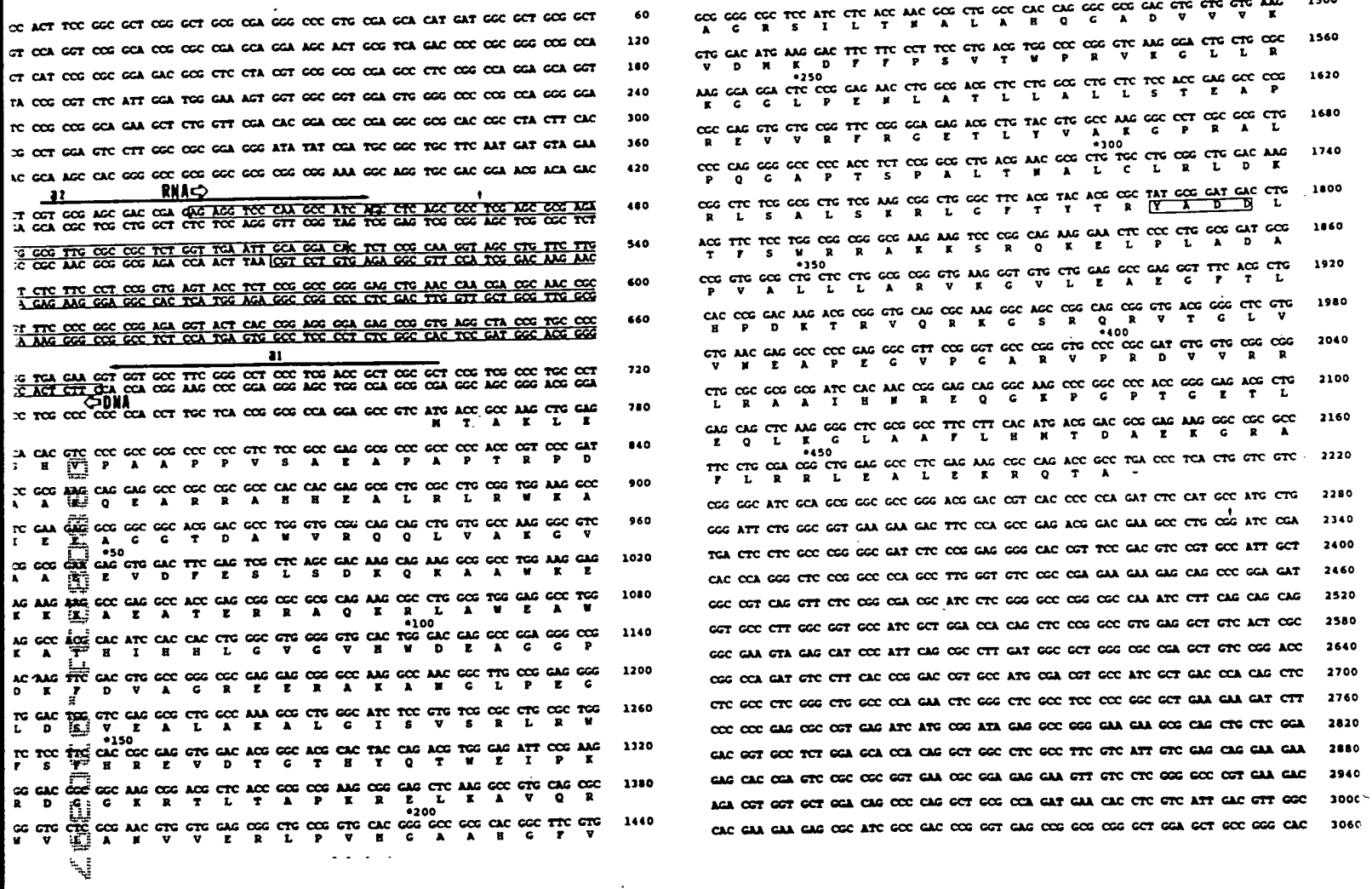


FIGURE 16

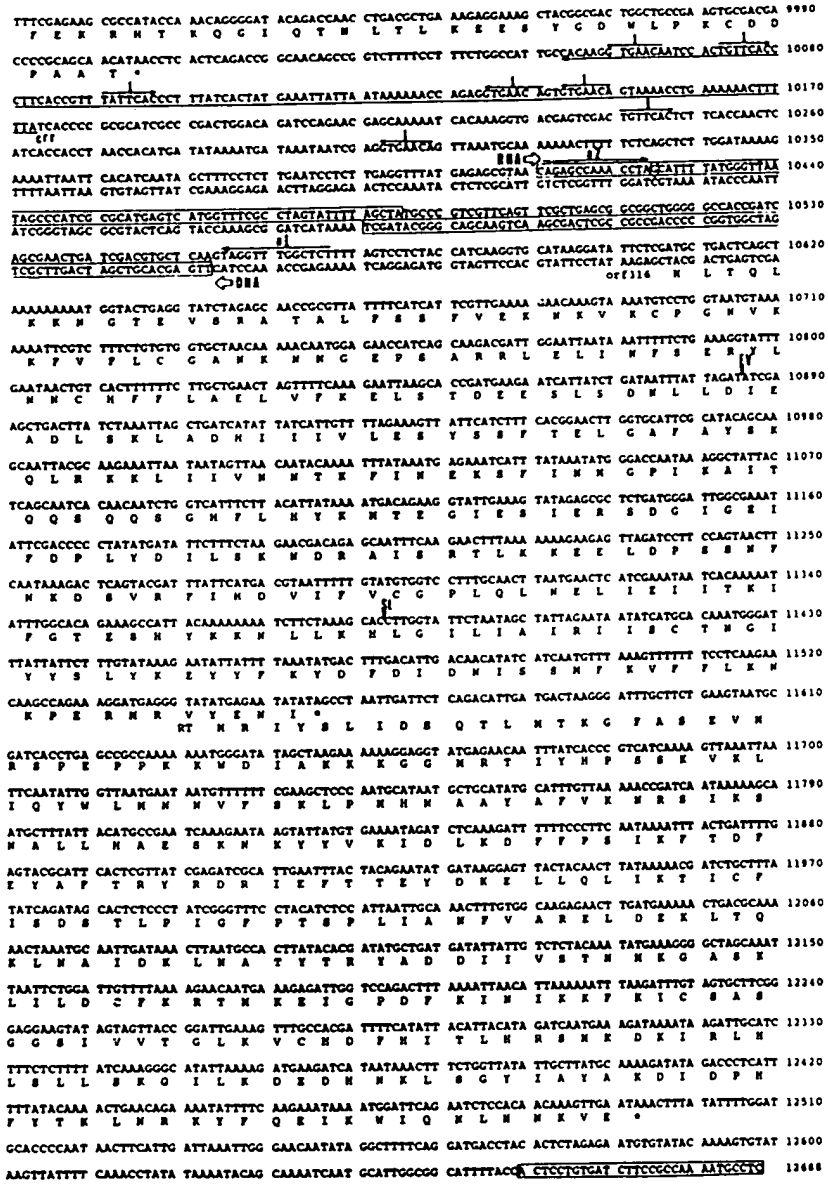
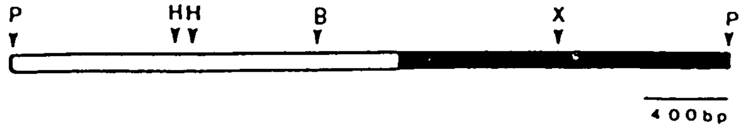


FIGURE 17

(A)




```
-371  TGGCATCTATTAAGAAGGTTAGGAAAGAAAATAAAGTATCAAAAGATATTGGAAATATAT

-311  TATACGCAGAGCGTTTCTATTGCCTTGTATCTATTTACTGGATAGTGTCAACTACCGCAC

-251  ACTGTGTGAACTAGCTTTTAAAGCGATAAAGCAAGATGATGTTTTATCTAAAATTATTGT

-191  TAGATCCGTTGTTTCTCGTCTAATAAATGAACGAAAAATACTTCAAATGACTGATGGTTA

-131  TCAGGTCACTGCTTTGGGGGCTAGCTATGTTAGGAGCGTCTTTGATAGAAAGACACTTGA

 -71  CCGATTGCGGCTTGAGATTATGAATTTTGAAAACCGTAGAAAATCAACATTTAACTATGA
                +1
               .|-|--------------------msdRNA----------------------
 -11  TAAGATTCCGTATGCGCACCCTTAGCGAGAGGTTTATCATTAAGGTCAACCTCTGGATGT
               IR ------------
      --------------------------------->
  49  TGTTTCGGCATCCTGCATTGAATCTGAGTTACTGTCTGTTTTCCTTGTTGGAACGGAGAG
                              <------------------------------------

 109  CATCGCCTGATGCTCTCCGAGCCAACCAGGAAACCCGTTTTTTCTGACGTAAGGGTGCGC
      ---------------------msDNA----------------------| -----------

 169  AACTTTCATGAAATCCGCTGAATATTTGAACACTTTTAGATTGAGAAATCTCGGCCTACC
      - IR    MetLysSerAlaGluTyrLeuAsnThrPheArgLeuArgAsnLeuGlyLeuPr

 229  TGTCATGAACAATTTGCATGACATGTCTAAGGCGACTCGCATATCTGTTGAAACACTTCG
      oValMetAsnAsnLeuHisAspMetSerLysAlaThrArgIleSerValGluThrLeuAr

 289  GTTGTTAATCTATACAGCTGATTTTCGCTATAGGATCTACACTGTAGAAAAGAAAGGCCC
      gLeuLeuIleTyrThrAlaAspPheArgTyrArgIleTyrThrValGluLysLysGlyPr

 349  AGAGAAGAGAATGAGAACCATTTACCAACCTTCTCGAGAACTTAAAGCCTTACAAGGATG
      oGluLysArgMetArgThrIleTyrGlnProSerArgGluLeuLysAlaLeuGlnGlyTr

 409  GGTTCTACGTAACATTTTAGATAAACTGTCGTCATCTCCTTTTTCTATTGGATTTGAAAA
      pValLeuArgAsnIleLeuAspLysLeuSerSerSerProPheSerIleGlyPheGluLy

 469  GCACCAATCTATTTTGAATAATGCTACCCCGCATATTGGGGCAAACTTTATACTGAATAT
      sHisGlnSerIleLeuAsnAsnAlaThrProHisIleGlyAlaAsnPheIleLeuAsnIl

 529  TGATTTGGAGGATTTTTTCCCAAGTTTAACTGCTAACAAAGTTTTTGGAGTGTTCCATTC
      eAspLeuGluAspPhePheProSerLeuThrAlaAsnLysValPheGlyValPheHisSe

 589  TCTTGGTTATAATCGACTAATATCTTCAGTTTTGACAAAAATATGTTGTTATAAAAATCT
      rLeuGlyTyrAsnArgLeuIleSerSerValLeuThrLysIleCysCysTyrLysAsnLe

 649  GCTACCACAAGGTGCTCCATCATCACCTAAATTAGCTAATCTAATATGTTCTAAACTTGA
      uLeuProGlnGlyAlaProSerSerProLysLeuAlaAsnLeuIleCysSerLysLeuAs

 709  TTATCGTATTCAGGGTTATGCAGGTAGTCGGGGCTTGATATATACGAGATATGCCGATGA
      pTyrArgIleGlnGlyTyrAlaGlySerArgGlyLeuIleTyrThrArgTyrAlaAspAs

 769  TCTCACCTTATCTGCACAGTCTATGAAAAAGGTTGTTAAAGCACGTGATTTTTTATTTTC
      pLeuThrLeuSerAlaGlnSerMetLysLysValValLysAlaArgAspPheLeuPheSe

 829  TATAATCCCAAGTGAAGGATTGGTTATTAACTCAAAAAAAACTTGTATTAGTGGGCCTCG
      rIleIleProSerGluGlyLeuValIleAsnSerLysLysThrCysIleSerGlyProAr

 889  TAGTCAGAGGAAAGTTACAGGTTTAGTTATTTCACAAGAGAAAGTTGGGATAGGTAGAGA
      gSerGlnArgLysValThrGlyLeuValIleSerGlnGluLysValGlyIleGlyArgGl

 949  AAAATATAAAGAAATTAGAGCAAAGATACATCATATATTTTGCGGTAAGTCTTCTGAGAT
      uLysTyrLysGluIleArgAlaLysIleHisHisIlePheCysGlyLysSerSerGluIl

1009  AGAACACGTTAGGGGATGGTTGTCATTTATTTTAAGTGTGGATTCAAAAAGCCATAGGAG
      eGluHisValArgGlyTrpLeuSerPheIleLeuSerValAspSerLysSerHisArgAr

1069  ATTAATAACTTATATTAGCAAATTAGAAAAAAAATATGGAAAGAACCCTTTAAATAAAGC
      gLeuIleThrTyrIleSerLysLeuGluLysLysTyrGlyLysAsnProLeuAsnLysAl

1129  GAAGACCTAATGGTCTTCGTTTTAAAACTAAAGCTCATAGGTTGAAAAATTGAGCACTTC
      aLysThr

1189  TTCGTCCAACCAGTTATTTAGTTCCTGCAATCGTTTCTGCAG
```

FIGURE 18

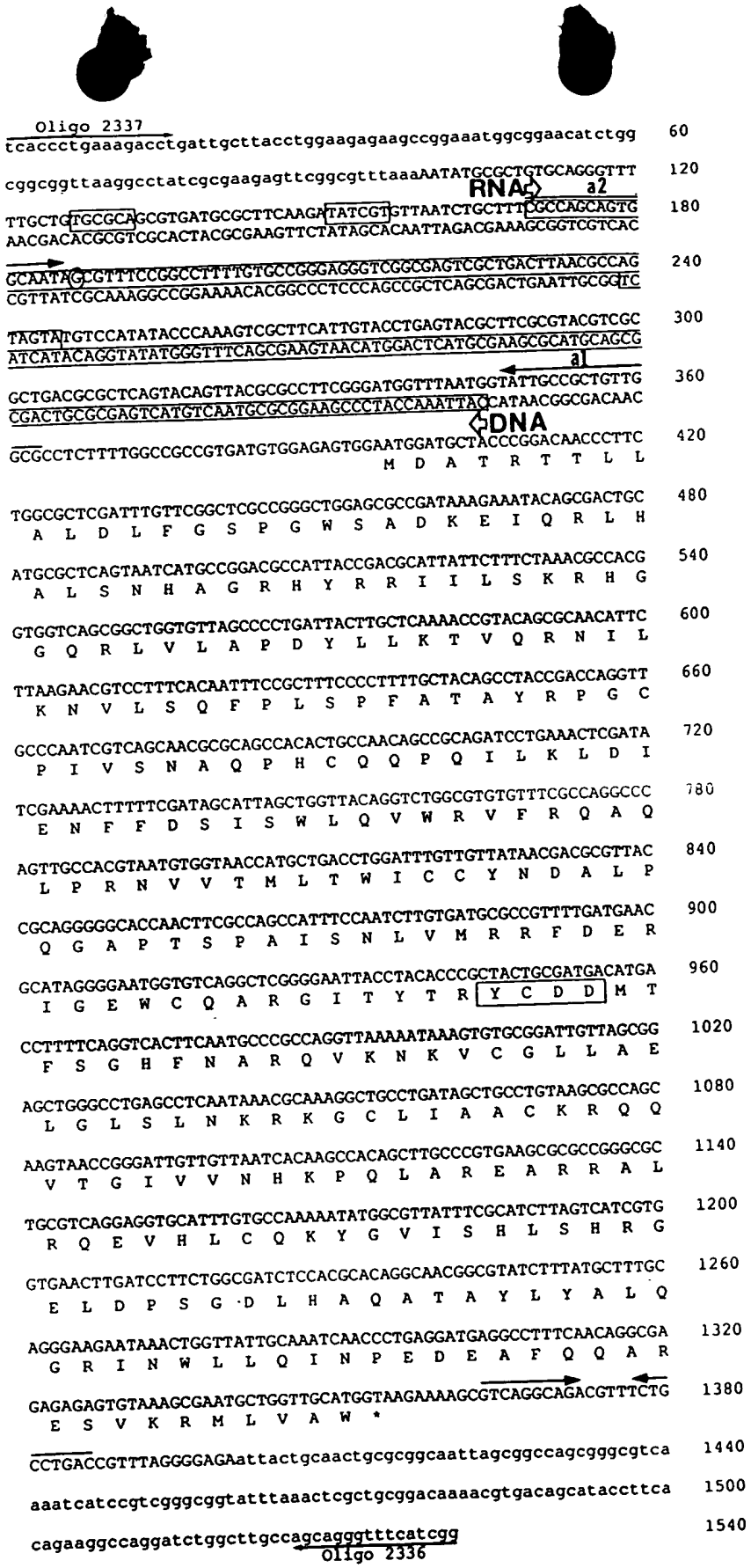


FIGURE 19

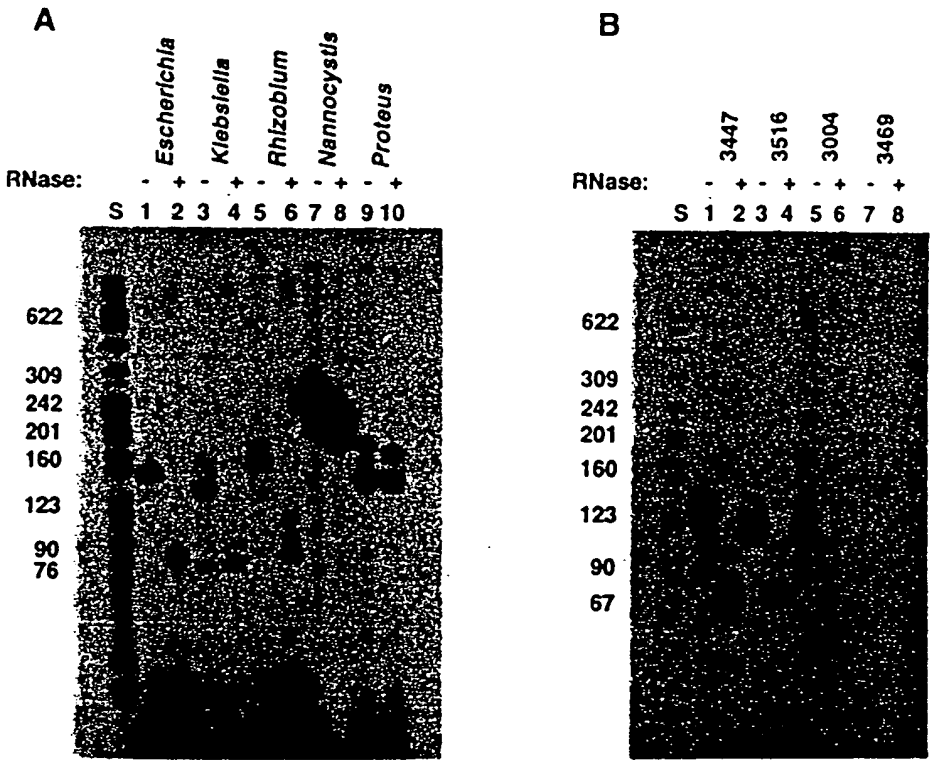

A
Escherichia
Klebsiella
Rhizobium
Nannocystis
Proteus
RNase: - + - + - + - + - +
S 1 2 3 4 5 6 7 8 9 10
622
309
242
201
160
123
90
76
B
3447
3516
3004
3469
RNase: - + - + - + - +
S 1 2 3 4 5 6 7 8
622
309
242
201
160
123
90
67

FIGURE 20

RHIZOBIAL ISOLATES

Strain (legume host genus)	USDA strain no.	Geographic source (date)	msDNA produced[b]
Rhizobium sp. (*Acacia*)	3002	Brazil (1959)	+
	3003	Africa (1950)	
	3325	Morocco (1974)	
	3838	? (1976)	+
Bradyrhizobium sp. (*Aeschynomene*)	3516	Florida (1972)	+
	4362		
Bradyrhizobium sp. (*Albizia*)	3004	Maryland (1952)	+
Bradyrhizobium sp. (*Apios*)	3240	Maryland (1939)	
Bradyrhizobium sp. (*Arachis*)	3339	Thailand (1979)	
	3341	Hawaii (1978)	
Rhizobium sp. (*Astragalus*)	3854	Alaska (1962)	
Rhizobium sp. (*Cajanus*)	3472		
Bradyrhizobium sp. (*Canavalia*)	3317	Brazil (1974)	
Rhizobium sp. (*Cicer*)	3378		
	3379	Mexico (1963)	
Bradyrhizobium sp. (*Coronilla*)	3165	Virginia (1935)	
	3167	? (1961)	
Bradyrhizobium sp. (*Crotalria*)	3384	Brazil (1967)	
Bradyrhizobium sp. (*Desmodium*)	3225	Ecuador (1948)	
Bradyrhizobium sp. (*Erythrina*)	3241		
	3242	Maryland (1939)	+
Rhizobium fredii	191	China (1979)	
Rhizobium leguminosarum	2370	Illinois (1933)	
	2429	Hawaii (1978)	
	2435	Holland (1955)	
	2480	Tennessee (1951)	
	2489		
Rhizobium sp. (*Lens*)	2426		
	3404	Colombia (1979)	
Rhizobium loti	3084	Maryland (1946)	
	3468	New Zealand (1961)	+
	3469		
	3471		
	3503		+
	3669	California (1968)	
Bradyrhizobium sp. (*Lotus*)	3074	Minnesota (1954)	
	3470	California (1916)	
Rhizobium sp. (*Lupinas*)	3040	Florida (1940)	
Bradyrhizobium sp. (*Lupinas*)	3045	Florida (1946)	
Bradyrhizobium sp. (*Macrotyloma*)	3451	Zimbabwe (1960)	
Rhizobium medicago	1097	North Dakota (1948)	
Rhizobium meliloti	1011	Maryland (1933)	
	1021a	North Dakota (1948)	
Rhizobium phaseoli	2667	Washington (1948)	
	2669		
	2674	Brazil (?)	
	2676	Colombia (1972)	
	3256	Illinois (1941)	
Rhizobium sp. (*Robinia*)	3436		
Bradyrhizobium sp. (*Stylosanthes*)	3441	Brazil (?)	
	3477	Colombia (1976)	
Rhizobium trifolii	2046	Virginia (1934)	
	2048	Illinois (1934)	+
	2063	Florida (1939)	
	2065	Alabama (1952)	+
	2116	South Carolina (1944)	
	2134	? (1974)	
	2145		
	2156	California (1920)	
Rhizobium sp. (*Trigonella*)	1177	Florida (1939)	
Rhizobium tropici	2744	Brazil (?)	
Bradyrhizobium sp. (*Vigna*)	3447	Thailand (1979)	+
	3456	Wisconsin (1966)	

[a] All strains are from the USDA Beltsville Rhizobium Culture Collection, provided by Peter van Berkum.
[b] As defined by detection of radiolabeled msDNA by the RT extension method.

FIGURE 21